



## (1) GENERAL INFORMATION:

(i) APPLICANT: Hewick, Rodney M.  
Wang, Jack H.  
Wozney, John M.  
Celeste, Anthony J.

(ii) TITLE OF INVENTION: Bone and Cartilage Inductive Proteins

(iii) NUMBER OF SEQUENCES: 14

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Legal Affairs, Genetics Institute, Inc.  
(B) STREET: 87 CambridgePark Drive  
(C) CITY: Cambridge  
(D) STATE: MA  
(E) COUNTRY: USA  
(F) ZIP: 02140

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/800,364  
(B) FILING DATE: 26-NOV-1991  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kapinos, Ellen J.  
(B) REGISTRATION NUMBER: 32,245  
(C) REFERENCE/DOCKET NUMBER: GI 5182A

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 617-876-1170  
(B) TELEFAX: 617-876-5851

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

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53 (iv) ANTI-SENSE: NO  
54  
55 (vi) ORIGINAL SOURCE:  
56 (F) TISSUE TYPE: Bone  
57  
58  
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
60  
61 Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp Trp  
62 1 5 10 15  
63  
64 Val Ile Ala Pro Gln Gly Tyr  
65 20  
66  
67 (2) INFORMATION FOR SEQ ID NO:2:  
68  
69 (i) SEQUENCE CHARACTERISTICS:  
70 (A) LENGTH: 18 amino acids  
71 (B) TYPE: amino acid  
72 (C) STRANDEDNESS: single  
73 (D) TOPOLOGY: unknown  
74  
75 (ii) MOLECULE TYPE: peptide  
76  
77 (iii) HYPOTHETICAL: NO  
78  
79 (iv) ANTI-SENSE: NO  
80  
81 (v) FRAGMENT TYPE: internal  
82  
83 (vi) ORIGINAL SOURCE:  
84 (A) ORGANISM: Bos taurus  
85 (F) TISSUE TYPE: Bone  
86  
87  
88 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
89  
90 Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile  
91 1 5 10 15  
92  
93 Leu Arg  
94  
95  
96 (2) INFORMATION FOR SEQ ID NO:3:  
97  
98 (i) SEQUENCE CHARACTERISTICS:  
99 (A) LENGTH: 7 amino acids  
100 (B) TYPE: amino acid  
101 (C) STRANDEDNESS: single  
102 (D) TOPOLOGY: unknown  
103  
104 (ii) MOLECULE TYPE: peptide

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105  
106 (iii) HYPOTHETICAL: NO  
107  
108 (iv) ANTI-SENSE: NO  
109  
110 (vi) ORIGINAL SOURCE:  
111 (A) ORGANISM: Bos taurus  
112 (F) TISSUE TYPE: Bone  
113  
114  
115 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
116  
117 Ala Cys Cys Ala Pro Thr Lys  
118 1 5  
119  
120 (2) INFORMATION FOR SEQ ID NO:4:  
121  
122 (i) SEQUENCE CHARACTERISTICS:  
123 (A) LENGTH: 23 amino acids  
124 (B) TYPE: amino acid  
125 (C) STRANDEDNESS: single  
126 (D) TOPOLOGY: unknown  
127  
128 (ii) MOLECULE TYPE: peptide  
129  
130 (iii) HYPOTHETICAL: NO  
131  
132 (vi) ORIGINAL SOURCE:  
133 (A) ORGANISM: Bos taurus  
134 (F) TISSUE TYPE: Bone  
135  
136  
137 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
138  
139 Thr Asn Glu Leu Pro Pro Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp  
140 1 5 10 15  
141  
142 Val His Gly Ser His Gly Arg  
143 20  
144  
145 (2) INFORMATION FOR SEQ ID NO:5:  
146  
147 (i) SEQUENCE CHARACTERISTICS:  
148 (A) LENGTH: 80 base pairs  
149 (B) TYPE: nucleic acid  
150 (C) STRANDEDNESS: double  
151 (D) TOPOLOGY: linear  
152  
153 (ii) MOLECULE TYPE: DNA (genomic)  
154  
155 (iii) HYPOTHETICAL: NO  
156

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157 (iv) ANTI-SENSE: NO  
158  
159 (vi) ORIGINAL SOURCE:  
160 (A) ORGANISM: Bos taurus  
161  
162 (vii) IMMEDIATE SOURCE:  
163 (B) CLONE: acc30  
164  
165 (viii) POSITION IN GENOME:  
166 (C) UNITS: bp  
167  
168 (ix) FEATURE:  
169 (A) NAME/KEY: CDS  
170 (B) LOCATION: 25..57  
171  
172  
173 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
174  
175 GGATCCGCGT GCTGTGCTCC GACC AAG CTG AGC GCC ACC TCC GTG CTC TAC 51  
176 Lys Leu Ser Ala Thr Ser Val Leu Tyr  
177 1 5  
178  
179 TAC GAC AGCAGCAACA ATGTAATTCT AGA 80  
180 Tyr Asp  
181 10  
182  
183  
184 (2) INFORMATION FOR SEQ ID NO:6:  
185  
186 (i) SEQUENCE CHARACTERISTICS:  
187 (A) LENGTH: 11 amino acids  
188 (B) TYPE: amino acid  
189 (D) TOPOLOGY: linear  
190  
191 (ii) MOLECULE TYPE: protein  
192  
193 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
194  
195 Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp  
196 1 5 10  
197  
198 (2) INFORMATION FOR SEQ ID NO:7:  
199  
200 (i) SEQUENCE CHARACTERISTICS:  
201 (A) LENGTH: 199 base pairs  
202 (B) TYPE: nucleic acid  
203 (C) STRANDEDNESS: double  
204 (D) TOPOLOGY: linear  
205  
206 (ii) MOLECULE TYPE: DNA (genomic)  
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208 (iii) HYPOTHETICAL: NO

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209  
210 (vi) ORIGINAL SOURCE:  
211 (A) ORGANISM: Bos Taurus  
212  
213 (vii) IMMEDIATE SOURCE:  
214 (A) LIBRARY: Bovine genomic  
215 (B) CLONE: Lambda 9800-10  
216  
217 (viii) POSITION IN GENOME:  
218 (C) UNITS: bp  
219  
220 (ix) FEATURE:  
221 (A) NAME/KEY: exon  
222 (B) LOCATION: 30..199  
223  
224 (ix) FEATURE:  
225 (A) NAME/KEY: intron  
226 (B) LOCATION: 1..29  
227  
228 (ix) FEATURE:  
229 (A) NAME/KEY: CDS  
230 (B) LOCATION: 30..179  
231  
232  
233 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:  
234  
235 TGCCCGCTGC CCCCTCCCGC CCCC GCCAG GTG CAC CTG CTG AAG CCG CAC GCG 53  
236 Val His Leu Leu Lys Pro His Ala  
237 1 5  
238  
239 GTC CCC AAG GCG TGC TGC GCG CCC ACC AAG CTG AGC GCC ACT TCC GTG 101  
240 Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val  
241 10 15 20  
242  
243 CTC TAC TAC GAC AGC AGC AAC AAC GTC ATC CTG CGC AAG CAC CGC AAC 149  
244 Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn  
245 25 30 35 40  
246  
247 ATG GTG GTC CGC GCC TGC GGC TGC CAC TGAGGCCCA ACTCCACCGG 196  
248 Met Val Val Arg Ala Cys Gly Cys His  
249 45 50  
250  
251 CAG 199  
252  
253  
254 (2) INFORMATION FOR SEQ ID NO:8:  
255  
256 (i) SEQUENCE CHARACTERISTICS:  
257 (A) LENGTH: 49 amino acids  
258 (B) TYPE: amino acid  
259 (D) TOPOLOGY: linear  
260

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261 (ii) MOLECULE TYPE: protein  
262  
263 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:  
264  
265 Val His Leu Leu Lys Pro His Ala Val Pro Lys Ala Cys Cys Ala Pro  
266 1 5 10 15  
267  
268 Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn  
269 20 25 30  
270  
271 Val Ile Leu Arg Lys His Arg Asn Met Val Val Arg Ala Cys Gly Cys  
272 35 40 45  
273  
274 His  
275  
276  
277  
278 (2) INFORMATION FOR SEQ ID NO:9:  
279  
280 (i) SEQUENCE CHARACTERISTICS:  
281 (A) LENGTH: 172 base pairs  
282 (B) TYPE: nucleic acid  
283 (C) STRANDEDNESS: double  
284 (D) TOPOLOGY: linear  
285  
286 (ii) MOLECULE TYPE: DNA (genomic)  
287  
288 (iii) HYPOTHETICAL: NO  
289  
290 (vi) ORIGINAL SOURCE:  
291 (A) ORGANISM: Bos taurus  
292  
293 (vii) IMMEDIATE SOURCE:  
294 (A) LIBRARY: Bovine genomic  
295 (B) CLONE: Lambda 9800-10  
296  
297 (viii) POSITION IN GENOME:  
298 (C) UNITS: bp  
299  
300 (ix) FEATURE:  
301 (A) NAME/KEY: exon  
302 (B) LOCATION: 51..161  
303  
304 (ix) FEATURE:  
305 (A) NAME/KEY: intron  
306 (B) LOCATION: 1..50  
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308 (ix) FEATURE:  
309 (A) NAME/KEY: intron  
310 (B) LOCATION: 162..172  
311  
312 (ix) FEATURE:

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313 (A) NAME/KEY: CDS  
314 (B) LOCATION: 51..161  
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316  
317 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:  
318  
319 GGGGTGGGAG GGCACGTGGA TGGGACTCAC CTTCTCCCAC TACCCCCCAG GAC TGG 56  
320 Asp Trp  
321 1  
322  
323 GTC ATC GCC CCC CAA GGC TAC TCA GCC TAT TAC TGT GAA GGG GAG TGC 104  
324 Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu Cys  
325 5 10 15  
326  
327 TCC TTC CCG CTG GAC TCC TGC ATG AAC GCC ACC AAC CAC GCC ATC CTG 152  
328 Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu  
329 20 25 30  
330  
331 CAG TCC CTG GTCAGTACCT C 172  
332 Gln Ser Leu  
333 35  
334  
335  
336 (2) INFORMATION FOR SEQ ID NO:10:  
337  
338 (i) SEQUENCE CHARACTERISTICS:  
339 (A) LENGTH: 37 amino acids  
340 (B) TYPE: amino acid  
341 (D) TOPOLOGY: linear  
342  
343 (ii) MOLECULE TYPE: protein  
344  
345 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:  
346  
347 Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly  
348 1 5 10 15  
349  
350 Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala  
351 20 25 30  
352  
353 Ile Leu Gln Ser Leu  
354 35  
355  
356 (2) INFORMATION FOR SEQ ID NO:11:  
357  
358 (i) SEQUENCE CHARACTERISTICS:  
359 (A) LENGTH: 119 base pairs  
360 (B) TYPE: nucleic acid  
361 (C) STRANDEDNESS: double  
362 (D) TOPOLOGY: linear  
363  
364 (ii) MOLECULE TYPE: DNA (genomic)

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365  
366 (iii) HYPOTHETICAL: NO  
367  
368 (vi) ORIGINAL SOURCE:  
369 (A) ORGANISM: Bos taurus  
370  
371 (vii) IMMEDIATE SOURCE:  
372 (A) LIBRARY: Bovine genous  
373 (B) CLONE: Lambda 9800-10  
374  
375 (viii) POSITION IN GENOME:  
376 (C) UNITS: bp  
377  
378 (ix) FEATURE:  
379 (A) NAME/KEY: exon  
380 (B) LOCATION: 20..99  
381  
382 (ix) FEATURE:  
383 (A) NAME/KEY: intron  
384 (B) LOCATION: 1..19  
385  
386 (ix) FEATURE:  
387 (A) NAME/KEY: intron  
388 (B) LOCATION: 100..119  
389  
390 (ix) FEATURE:  
391 (A) NAME/KEY: CDS  
392 (B) LOCATION: 22..99  
393  
394  
395 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:  
396  
397 CCCTTGCGTG TCCCCGCAGA C GAC GTC CAC GGC TCC CAC GGC CGG CAG GTG 51  
398 Asp Val His Gly Ser His Gly Arg Gln Val  
399 1 5 10  
400  
401 TGC CGT CGG CAC GAG CTG TAC GTG AGC TTC CAG GAC CTG GGC TGG CTG 99  
402 Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu  
403 15 20 25  
404  
405 GTGAGTTCCG ACTCTCCTTT 119  
406  
407  
408 (2) INFORMATION FOR SEQ ID NO:12:  
409  
410 (i) SEQUENCE CHARACTERISTICS:  
411 (A) LENGTH: 26 amino acids  
412 (B) TYPE: amino acid  
413 (D) TOPOLOGY: linear  
414  
415 (ii) MOLECULE TYPE: protein  
416



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417 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

418  
419 Asp Val His Gly Ser His Gly Arg Gln Val Cys Arg Arg His Glu Leu  
420 1 5 10 15421  
422 Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu  
423 20 25424  
425 (2) INFORMATION FOR SEQ ID NO:13:426  
427 (i) SEQUENCE CHARACTERISTICS:

428 (A) LENGTH: 1003 base pairs

429 (B) TYPE: nucleic acid

430 (C) STRANDEDNESS: double

431 (D) TOPOLOGY: circular

432

433 (ii) MOLECULE TYPE: cDNA to mRNA

434

435 (iii) HYPOTHETICAL: NO

436

437 (vi) ORIGINAL SOURCE:

438 (A) ORGANISM: Homo sapiens

439 (F) TISSUE TYPE: Human Heart

440

441 (vii) IMMEDIATE SOURCE:

442 (A) LIBRARY: Human heart cDNA library stratagene catalog  
443 #936208

444 (B) CLONE: hh38

445

446 (viii) POSITION IN GENOME:

447 (C) UNITS: bp

448

449 (ix) FEATURE:

450 (A) NAME/KEY: CDS

451 (B) LOCATION: 8..850

452

453 (ix) FEATURE:

454 (A) NAME/KEY: mat\_peptide

455 (B) LOCATION: 427..843

456

457 (ix) FEATURE:

458 (A) NAME/KEY: mRNA

459 (B) LOCATION: 1..997

460

461

462 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

463

464 GAATTCC GAG CCC CAT TGG AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC 49

465 Glu Pro His Trp Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile

466 -139 -135 -130

467

468 CCG GCT GGG GAG GCG GTC ACA GCT GCG GAG TTC CGG ATT TAC AAG GTG 97

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469	Pro	Ala	Gly	Glu	Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Val	
470	-125					-120				-115						-110	
471																	
472	CCC	AGC	ATC	CAC	CTG	CTC	AAC	AGG	ACC	CTC	CAC	GTC	AGC	ATG	TTC	CAG	145
473	Pro	Ser	Ile	His	Leu	Leu	Asn	Arg	Thr	Leu	His	Val	Ser	Met	Phe	Gln	
474					-105					-100						-95	
475																	
476	GTG	GTC	CAG	GAG	CAG	TCC	AAC	AGG	GAG	TCT	GAC	TTG	TTC	TTT	TTG	GAT	193
477	Val	Val	Gln	Glu	Gln	Ser	Asn	Arg	Glu	Ser	Asp	Leu	Phe	Phe	Leu	Asp	
478				-90					-85						-80		
479																	
480	CTT	CAG	ACG	CTC	CGA	GCT	GGA	GAC	GAG	GGC	TGG	CTG	GTG	CTG	GAT	GTC	241
481	Leu	Gln	Thr	Leu	Arg	Ala	Gly	Asp	Glu	Gly	Trp	Leu	Val	Leu	Asp	Val	
482			-75					-70					-65				
483																	
484	ACA	GCA	GCC	AGT	GAC	TGC	TGG	TTG	CTG	AAG	CGT	CAC	AAG	GAC	CTG	GGA	289
485	Thr	Ala	Ala	Ser	Asp	Cys	Trp	Leu	Leu	Lys	Arg	His	Lys	Asp	Leu	Gly	
486	-60						-55				-50						
487																	
488	CTC	CGC	CTC	TAT	GTG	GAG	ACT	GAG	GAT	GGG	CAC	AGC	GTG	GAT	CCT	GGC	337
489	Leu	Arg	Leu	Tyr	Val	Glu	Thr	Glu	Asp	Gly	His	Ser	Val	Asp	Pro	Gly	
490	-45					-40				-35						-30	
491																	
492	CTG	GCC	GGC	CTG	CTG	GGT	CAA	CGG	GCC	CCA	CGC	TCC	CAA	CAG	CCT	TTC	385
493	Leu	Ala	Gly	Leu	Leu	Gly	Gln	Arg	Ala	Pro	Arg	Ser	Gln	Gln	Pro	Phe	
494				-25					-20					-15			
495																	
496	GTG	GTC	ACT	TTC	TTC	AGG	GCC	AGT	CCG	AGT	CCC	ATC	CGC	ACC	CCT	CGG	433
497	Val	Val	Thr	Phe	Phe	Arg	Ala	Ser	Pro	Ser	Pro	Ile	Arg	Thr	Pro	Arg	
498			-10					-5						1			
499																	
500	GCA	GTG	AGG	CCA	CTG	AGG	AGG	AGG	CAG	CCG	AAG	AAA	AGC	AAC	GAG	CTG	481
501	Ala	Val	Arg	Pro	Leu	Arg	Arg	Arg	Gln	Pro	Lys	Lys	Ser	Asn	Glu	Leu	
502		5					10					15					
503																	
504	CCG	CAG	GCC	AAC	CGA	CTC	CCA	GGG	ATC	TTT	GAT	GAC	GTC	CAC	GGC	TCC	529
505	Pro	Gln	Ala	Asn	Arg	Leu	Pro	Gly	Ile	Phe	Asp	Asp	Val	His	Gly	Ser	
506	20					25					30					35	
507																	
508	CAC	GGC	CGG	CAG	GTC	TGC	CGT	CGG	CAC	GAG	CTC	TAC	GTC	AGC	TTC	CAG	577
509	His	Gly	Arg	Gln	Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val	Ser	Phe	Gln	
510					40					45					50		
511																	
512	GAC	CTT	GGC	TGG	CTG	GAC	TGG	GTC	ATC	GCC	CCC	CAA	GGC	TAC	TCA	GCC	625
513	Asp	Leu	Gly	Trp	Leu	Asp	Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser	Ala	
514				55					60					65			
515																	
516	TAT	TAC	TGT	GAG	GGG	GAG	TGC	TCC	TTC	CCG	CTG	GAC	TCC	TGC	ATG	AAC	673
517	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser	Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	
518			70					75					80				
519																	
520	GCC	ACC	AAC	CAC	GCC	ATC	CTG	CAG	TCC	CTG	GTG	CAC	CTG	ATG	AAG	CCA	721

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521 Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro  
522 85 90 95  
523  
524 AAC GCA GTC CCC AAG GCG TGC TGT GCA CCC ACC AAG CTG AGC GCC ACC 769  
525 Asn Ala Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr  
526 100 105 110 115  
527  
528 TCT GTG CTC TAC TAT GAC AGC AGC AAC AAC GTC ATC CTG CGC AAG CAC 817  
529 Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His  
530 120 125 130  
531  
532 CGC AAC ATG GTG GTC AAG GCC TGC GGC TGC CAC TGAGTCAGCC CGCCCAGCCC 870  
533 Arg Asn Met Val Val Lys Ala Cys Gly Cys His  
534 135 140  
535  
536 TACTGCAGCC ACCCTTCTCA TCTGGATCGG GCCCTGCAGA GGCAGAAAAC CCTTAAATGC 930  
537  
538 TGTCACAGCT CAAGCAGGAG TGTCAGGGGC CCTCACTCTC GGTGCCTACT TCCTGTCAGG 990  
539  
540 CTTCTGGGAA TTC 1003  
541  
542  
543 (2) INFORMATION FOR SEQ ID NO:14:  
544  
545 (i) SEQUENCE CHARACTERISTICS:  
546 (A) LENGTH: 281 amino acids  
547 (B) TYPE: amino acid  
548 (D) TOPOLOGY: linear  
549  
550 (ii) MOLECULE TYPE: protein  
551  
552 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:  
553  
554 Glu Pro His Trp Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala  
555 -139 -135 -130 -125  
556  
557 Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser  
558 -120 -115 -110  
559  
560 Ile His Leu Leu Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val  
561 -105 -100 -95  
562  
563 Gln Glu Gln Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln  
564 -90 -85 -80  
565  
566 Thr Leu Arg Ala Gly Asp Glu Gly Trp Leu Val Leu Asp Val Thr Ala  
567 -75 -70 -65 -60  
568  
569 Ala Ser Asp Cys Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu Arg  
570 -55 -50 -45  
571  
572 Leu Tyr Val Glu Thr Glu Asp Gly His Ser Val Asp Pro Gly Leu Ala

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```
573          -40          -35          -30
574
575 Gly Leu Leu Gly Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val
576          -25          -20          -15
577
578 Thr Phe Phe Arg Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg Ala Val
579          -10          -5          1          5
580
581 Arg Pro Leu Arg Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln
582          10          15          20
583
584 Ala Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly
585          25          30          35
586
587 Arg Gln Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu
588          40          45          50
589
590 Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr
591          55          60          65
592
593 Cys Glu Gly Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr
594          70          75          80          85
595
596 Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala
597          90          95          100
598
599 Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val
600          105          110          115
601
602 Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn
603          120          125          130
604
605 Met Val Val Lys Ala Cys Gly Cys His
606          135          140
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PAGE: 1

SEQUENCE VERIFICATION REPORT  
PATENT APPLICATION US/07/800,364A

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S3925

LINE ERROR

ORIGINAL TEXT

27 Wrong application Serial Number  
443 Response Exceeds Line Limitations

(A) APPLICATION NUMBER: US 07/800,364  
#936208



PAGE:

1

SEQUENCE MISSING ITEM REPORT  
PATENT APPLICATION US/07/800,364A

DATE: 01/04/93  
TIME: 14:24:31  
S3925

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA  
APPLICATION NUMBER  
FILING DATE

PAGE: 1

SEQUENCE CORRECTION REPORT  
PATENT APPLICATION US/07/800,364A

DATE: 01/04/93  
TIME: 14:24:31  
S3925

LINE ORIGINAL TEXT

CORRECTED TEXT